

GenCore version 5.1.3	Copyright (c) 1993 - 2003 Compugen Ltd.	Sequence 2332, Ap
OM nucleic - nucleic search, using sw model		Sequence 4448, Ap
Run on:	February 16, 2003, 22:05:25 ; search time 51.2985 Seconds (without alignments) 13999.354 Million cell updates/sec	Sequence 8394, Ap
Title:	US-09-497-967-44	Sequence 50, Appl
Perfect score:	1410	Sequence 84, Appl
Sequence:	1 atgaaaaataatttttagt.cttattttttttatgtga 1410	Sequence 143, Appl
Scoring table:	IDENTITY_NUC	Sequence 86, Appl
	Gapop 10.0 , Gapext 1.0	Sequence 10113, A
Searched:	424239 seqs, 254661826 residues	Sequence 4857, Ap
Total number of hits satisfying chosen parameters:	848478	Sequence 8774, Ap
Minimum DB seq length:	0	Sequence 9048, Ap
Maximum DB seq length:	2000000000	Sequence 2, Appl
Post-processing:	Minimum Match 0%	Sequence 1, Appl
	Maximum Match 100%	Sequence 6, Appl
	Listing first 45 summaries	Sequence 3136, Ap
Database :	Published_Applications_NA: *	Sequence 10, Appl
	1: /cgns_6/podata/1/pubnra/US07_PUBCOMB.seq;*	Sequence 40, Appl
	2: /cgns_6/podata/1/pubnra/PC7_NEW_PUB.seq;*	Sequence 13, Appl
	3: /cgns_6/podata/1/pubnra/PC6_NEW_PUB.seq;*	Sequence 14, Appl
	4: /cgns_6/podata/1/pubnra/US06_PUBCOMB.seq;*	Sequence 7, Appl
	5: /cgns_6/podata/1/pubnra/US07_PUBCOMB.seq;*	Sequence 2937, Ap
	6: /cgns_6/podata/1/pubnra/PC105_PUBCOMB.seq;*	Sequence 1, Appl
	7: /cgns_6/podata/1/pubnra/US10_PUB.seq;*	Sequence 6, Appl
	8: /cgns_6/podata/1/pubnra/US08_PUB.seq;*	Sequence 33, Ap
	9: /cgns_6/podata/1/pubnra/US09_PUBCOMB.seq;*	Sequence 27, Ap
	10: /cgns_6/podata/1/pubnra/US09_PUBCOMB.seq;*	Sequence 402, Ap
	11: /cgns_6/podata/1/pubnra/US10_NEW_PUB.seq;*	Sequence 28, Ap
	12: /cgns_6/podata/1/pubnra/US10_PUBCOMB.seq;*	Sequence 29, Ap
	13: /cgns_6/podata/1/pubnra/US50_NEW_PUB.seq;*	Sequence 30, Ap
	14: /cgns_6/podata/1/pubnra/US50_PUBCOMB.seq;*	Sequence 31, Ap
Pred.	No. Is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	Sequence 32, Ap
		SEQUENCES
Result No.	Score	Query Length DB ID Description
C 1	60	4.3 1635 10 US-09-864-761-20241 Sequence 20241, A
C 2	60	4.3 1973 10 US-09-864-761-3471 Sequence 3471, Ap
C 3	52.2	3.7 510 10 US-09-864-761-8737 Sequence 18737, A
C 4	46.6	3.3 684 973 10 US-09-864-761-9591 Sequence 19241, A
C 5	45.8	3.3 1075 10 US-09-864-761-19241 Sequence 2513, Ap
C 6	45.8	3.2 1403 10 US-09-864-761-2513 Sequence 95, Appl
C 7	43.4	3.1 2120 10 US-09-798-042-95 Sequence 39, Appl
C 8	43.4	3.1 2129 10 US-09-159-469-9 Sequence 39, Appl
C 9	43.4	3.1 2129 10 US-09-798-042-39 Sequence 20174, A
C 10	42.8	3.0 439 10 US-09-864-761-20174 Sequence 20174, A
C 11	42.6	3.0 1390 10 US-09-970-477-1 Sequence 1, Appl
C 12	42.6	3.0 25002 9 US-10-024-623-31 Sequence 31, Appl
C 13	42	3.0 574 10 US-09-864-761-228 Sequence 3228, App
C 14	41.4	2.9 1881 9 US-09-938-842A-3346 Sequence 3346, Ap
C 15	41	2.9 489 10 US-09-864-761-4976 Sequence 4976, Ap
C 16	40.4	2.9 1476 10 US-09-815-242-8766 Sequence 8766, Ap
C 17	40.4	2.9 4460 10 US-09-740-274-1 Sequence 1, Appl
C 18	40	2.8 250 10 US-09-815-242-3253 Sequence 3253, Ap
C 19	40	2.8 250 10 US-09-815-242-3273 Sequence 3273, Ap

ALIGNMENTS

RESULT 1
US-09-864-761-20241/c
; Sequence 20241, Application US-09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenseng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR MICROARRAY EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US-09-864-761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00671
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00672
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00673
; PRIOR FILING DATE: 2001-01-30

RESULT 5
 ; Sequence 19241, Application US/09864761
 ; Patent No. US20020018763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Aeonimica-X-11
 ; CURRENT APPLICATION NUMBER: US/09/7864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263 . 6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR FILING DATE: 2001-01-30

Qy 640 TGTCCGGCAATTAAACCTCTTAAGCTTAAGTGTGTTAACATA 699
 Db 13221 TCCCCCTACAAAATACTGCGATGCGATTAACCTATGCCCT 13280
 Qy 700 ACCGCGATAATGTAAGCTTCATGCCCTGAGTACTAATGCTGAGCTAAATAAT 759
 Db 13281 TCTCTTACAGTAGTACTACTGTGAGTACTATGCTACCTGACCTCCT 13340
 Qy 760 TGGTAGCACAAACACTGAAATGTAATGCTCAACTTITACATAATAATGCT 819
 Db 13341 TCTCTGACAGTAGTACTGCTGATGCCACCATAGTACTGCTACTCTCCT 13400
 Qy 820 CCTAATTCGAATCCAGTAATGACTACATGCCPACCTGCCGCAATAAGATTATGGT 879
 Db 13401 TCTCTAACAGGTACTACGTGTTAGCCTACTATAGTACTCTCCT 13460
 Qy 880 GCTGAAGCCACTCGAGGTGTCGGCTACTTTAGCCAATAATGTAATGCTGCCT 939
 Db 13461 GTTCAAACAAATACTACTATGTTAGCACTAGTACTATGCTCTAC 13520
 Qy 940 GATGGTACTGCAATTGCTGATGTGAGCAACTAAATTATGTAATTTAAACAGAAATGCTCA 999
 Db 13521 TCATCATACAAAGTACTGTGATCTCTTAACTACTGTCAGTACGCTATCCR 13580
 Qy 1000 AATTGTGCTGCTA 1012
 Db 13581 TCTCTTGAAATA 13563

Qy 288 TGATGCTACCGCAATTGGCGAGTGGCGACAGATTTGAGCCTATACAGAATGCT 347
 Db 216 TGATGCTGGTGTGATGGTGGTGTGCTGATGGTGGTGTGATGGTGGTGG 275
 Qy 348 TAATGCTGAGTTANTTTATAATGAAATGCPCCAATAATTAAATGAGGTGTAATGCTAC 407
 Db 276 TGGTGTATGGTGTGATGGTGTGATGGTGTGATGGTGTGATGGTGTGATGGTGG 325
 Qy 408 ATGCCACCGTGTGGTAAACAGCTGGTGAATTGACTGTGTAATGGCTCATAC 467
 Db 336 TGGTGTGGTGTGATGGTGTGATGGTGTGATGGTGTGATGGTGTGATGGTGTGTA 395
 Qy 468 CATAGTCGATAATGTAACGTGCGATGTCCTACTGGTACTGGACTTGTGACPAR 527
 Db 396 TGGTGTGGTGTGATGGTGTGATGGTGTGATGGTGTGATGGTGTGATGGTGG 455
 Qy 528 TACTGATTATGTTAGTCACTTACAGAAATGTTAAAGTAGCTTACTTACTATAA 587
 Db 456 TGGTGTGGTGTGATGGTGTGATGGTGTGATGGTGTGATGGTGTGATGGTGG 515
 Qy 588 TGGTAATAATGTTAATCTCTTCATGAACTTGTGCTGCG 647
 Db 516 TGGTGTGGTGTGATGGTGTGATGGTGTGATGGTGTGATGGTGTGATGGTGG 575
 Qy 648 AATTAAACCTGTCAATTGCTTAAGCTTACTTTAGTTAATGTCATAAATACCGATA 707
 Db 576 TAGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 635
 Qy 708 ATGTAACCTGTGATGCCCTGATGGTACTATAATGCTGCTGGTAAATAATGGTGGAGC 767
 Db 636 TGGTGTGGTGTGATGGTGTGATGGTGTGATGGTGTGATGGTGTGGTGTGG 695
 Qy 768 ACAAAACACTGAAATGTAATGCTGCTCAACTTTACAATAATGCTGCTGGTAAATAATGGTGGAGC 827
 Db 696 TGGTGTGGTGTGATGGTGTGATGGTGTGATGGTGTGATGGTGTGGTGTGGTGTGG 755
 Qy 828 CAATCCAGTAATAGTACATGCCCTACCTGCCAGCAAAATAAGATAATGGTGTGGTGTGGAGC 887
 Db 756 TGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGG 815
 Qy 888 CACTGCAAGGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTAC 947

Query Match Score 45.8; DB 10; Length 1075;
 Best Local Similarity 3.2%; Score 45.8;
 Matches 287; Conservative 0; Mismatches 402; Indels 0; Gaps 0;

OTHER INFORMATION: MAP TO AL078472.1
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 27
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 19
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 34
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 7.1
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 28
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 43
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 20
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 25
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 18
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 21
 OTHER INFORMATION: EST-HUMAN HIT: AV739739.1, EVALU 1.00e+00
 OTHER INFORMATION: NT HIT: AL163201.2, EVALU 2.00e-19

US-09-864-761-19241
 US-09-864-761-19241

RESULT 6

Db	816	TCATGGTGTGGCTGGGGCATGGTTTAGTGATGCGTGGTAG 875
Qy	948	TGCAATTGCTAGTGACCAACTATATG 976
Db	876	TGGGTGTGGTGTAGTGTTAGTGCTGGTAG 904

; Sequence 2513, Application US/09864761
; Patient No. US20030048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Weisheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemola-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annamax Sequence Listing Engine vers. 1.1
; SEQ ID NO: 2513
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL078472.1 MARROW, SIGNAL = 27
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 19
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 34
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 7.1
; OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 28
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 4.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 20

SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 95
 LENGTH: 2120
 TYPE: DNA
 ORGANISM: Ehrlichia
 US-09-798-042-95

Query Match Score 3.1%; DB 10; Length 2120;
 Best Local Similarity 44.3%; Pred. No. 0; Mismatches 336; Indels 12; Gaps 2;

Query	Subject	Score	DB	Length
Qy 287	CAGCTGGTACCGAAATTCAGGCAACAGATTATGGGCAATANTCACAGAATG	3.18	43.4	2120
Db 1502	CTTCCTCTGCATACAGCATAGCTTCAGAATCTAGATCACCTCTAG	4.38	58	2120
Qy 347	TAAATGTGAAATTAAATTATAATGAAATAATGCTCAAAATTAAATGAGGTCTAGTAGTA	4.06	0	2120
Db 1442	TAACCCAAGAACGTAGACTCAGGCTGGCGAGAAACPTCAGGCTGATTC	4.06	336	2120
Qy 407	CATGCACAGCCTGTCGGTAAACAGATTGTTGCGTCAATTGACTGCTGSTAATGCCGCTA	3.46	58	2120
Db 1382	GTTGTTGCGCTCTGGAGCAACTACCACCTCTGAAAGCTTATTTCTCTAGTGATGTTA	4.66	12	2120
Qy 467	CCATAGTCGATAAATGAACTGCGATGTCCTACTGTACTGTGAGGATPA	5.26	39	2120
Db 1322	CAATCCTCTGCAGGTTAACACAGGAATTCTGCTCAGTACTACAGGACTCTGTG	5.26	39	2120
Qy 527	CTACTGATTATGTTAGATCATTACAGAATGTTGAGATTAACTTTACT	5.83	39	2120
Db 1262	CTACAGGTTGCTCAGATCTCAAGATCTCAAGATCTCTCTTAAAGCTCCT	5.83	39	2120
Qy 584	ATAATGTTAAATGGTAATCTCCTCAATCCAGGTAAGGTTAAATGTTAATGCAACCTGTC	6.43	39	2120
Db 1202	TTACPTCTAGGGACCTTCAGTTCCCTCTAGTCAGCTTCAGCAATTCTGCTTGTGAC	6.43	39	2120
Qy 644	CGGCAAATTAAACCTGCTTAATGTTGCTTAAGCTACTTAACTGATGCTACAATACCG	7.03	39	2120
Db 1142	CAGAGTAACTTCTTTCGGCFACATCAGGATTAGCTTCTAGATGACTTCAGACTTTA	7.03	39	2120
Qy 704	CATAATGTAACGTGCAATGCCNAGTACTATAATGCTGCTGGTAATAATGG	7.63	39	2120
Db 1082	GATCACCTCAGCAACCAAGAACGTAAGCTGAGCTCAGGTTGTCGGCAGAACCTCG	10.23	39	2120
Qy 764	TAGCACAAAACCTGAATGTTGACTAATTTGCTCTTAACATTAAATGGCTCTA	8.23	39	2120
Db 1022	GAG-----CTGATCTAGTTGTCGCTCTGGAGCAACTACCAACTCTGAAAGCT	9.72	39	2120
Qy 824	ATTATCAATCCAGGAAATAGTACATGCCCTACCTTGCCAGCAATAAAGATATTGTCGT	8.83	39	2120
Db 971	TATTTCTCTAGTGAATGTTGACATCCTCTGAGCTTAAACACAGGTAATTCTGCT	9.12	39	2120
Qy 884	AAGCCACATGCGGGGCCGTAC	9.08	39	2120
Db 911	CAGCTACTACAGGTACTTGCGCTAC	8.87	39	2120

RESULT 8
US-09-159-469-39
Sequence 39, Application US/09159469
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF INFECTION: THERAPY OF EHRLICHIA INFECTION
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA

ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATOR: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/159,469
FILING DATE:
CLASSIFICATION:
PRIVOR APPLICATION DATA:
APPLICATION NUMBER: 09/106,582
FILING DATE: 29-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121,439C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 2129 base Pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-159-469-39

Query Match Score 3.1%; DB 10; Length 2129;
Best Local Similarity 44.3%; Pred. No. 0; Mismatches 336; Indels 12; Gaps 27;
Matches 27;

Query	Subject	Score	DB	Length
Qy 287	CTGCCTGGTACCGCAATTGCGAGGAAACAGATTATGGGCAATANTCACAGAATG	3.18	43.4	2129
Db 619	CTTCFTGCTGTCAGGATCTACAGATCTACAGTACTCTGAGCTTCACTCTCAG	4.66	58	2129
Qy 347	TAAATGTGAAATTAAATTATAATGAAATAATGGCTTAAATTTGAGGTGCTAGTA	5.26	39	2129
Db 679	TAACACCAAAACTCTAGACTCAGGTTGTCGTGAGGCTGATCTCACTGATCTCA	5.26	39	2129
Qy 407	CATGCAGCCTGTCGGTAACAGAGTTGCTGTTGAGCTTAATGCTGCTTGTGTC	6.43	39	2129
Db 739	GTTCGTGCGCTTCGGAGAACCTACCACTCTCTGAACTTATTTCTCTAGTGTGTA	6.43	39	2129
Qy 467	CCATAGTCGATATGTTACGTCGATGCTCCATGCTCTACTGGTACTGCTAGTGT	7.03	39	2129
Db 799	CAACGGCTTCGAGCTCAACACAGTAATCTGCTTGTGCTGCTGCTGCTGCTG	7.03	39	2129
Qy 527	CTAGTGAATATGCTTAAGCTGCTTAAGCTTAATGCTGCTTGTGCTGCTGCTG	7.63	39	2129
Db 859	CTAGGGTTGTCGCTCAAGAATCTAAAGTCTCTGCTTGTGCTGCTGCTGCTG	7.63	39	2129
Qy 584	ATAATGCTAATAATGCTTAATCTGCTTAAGCTGCTTGTGCTGCTGCTGCTG	8.23	39	2129
Db 919	TTACTTCGACAGGAGCTTCAGCTCTAGCTCTGCTTGTGCTGCTGCTGCTG	8.23	39	2129
Qy 644	CGGAAATTAAACCTGCTTAATGCTCTTAACATTAAATGGCTCTA	8.83	39	2129
Db 979	CAGAGTAACTCTGCTTGTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG	8.83	39	2129
Qy 704	CATAATGTAACGTGCAATGCCNAGTACTATAATGCTGCTGGTAATAATGG	9.08	39	2129
Db 1039	GATCACCTCAGCAACCAAGAACCTGAGCTCAGGTTGTCGCTGCTGCTGCTG	9.08	39	2129
Qy 764	TAGCACAAAACCTGAATAGTACATGCCCTACCTTGCCAGCAATAAAGATATTGTC	9.12	39	2129
Db 1099	GAG-----CTGATCTCTAGTTGTCGCTTGTGCTGCTGCTGCTGCTGCTG	9.12	39	2129
Qy 824	ATTCAATCCAGGAACTCTGCTTAATGCTCTAAGCTGCTTGTGCTGCTGCTG	9.23	39	2129
Db 1150	TATTTCTCTAGTTGTCGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG	9.23	39	2129

RESULT 15
us-09-864-761-4976/C

; Sequence: Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wenshang

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeom1-X-1
; CURRENT APPLICATION NUMBER: US/09/864 761

; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180, 312
; PRIORITY FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIORITY FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIORITY FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263, 6
; PRIORITY FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIORITY FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIORITY FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIORITY FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIORITY FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIORITY FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIORITY FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIORITY FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIORITY FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIORITY FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIORITY FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIORITY FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234, 687
; PRIORITY FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608, 408
; PRIORITY FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax sequence Listing Engine vers. 1.1
; SEQ ID NO: 4976
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL031076.1
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 5.1
; OTHER INFORMATION: EXPRESSED IN HEIA, SIGNAL = 5.2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.1

; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.9
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.4
; US-09-864-761-4976

Query Match 2.9%; Score 41; DB 10; Length 489;
Best Local Similarity 50.2%; Pred. No. 1.2;
Matches 101; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

Qy 339 AGATGTTAAATTGAGAATTATTTTATGCAAATTTAATGCATA 656
Db 379 ATATGGATAATGGTAATGGCATGATAATGGTAATCATGGTGTATGG 320

Qy 399 TGTAGTACATGGACAGTTGTTGTCATGACTGCTGTAA 458
Db 319 TGTTGATTATGGTAGGATGGATGATAATGGTGTGGATGGATGGTGA 260

Qy 459 TGCGGTACCATAGTCGATAATGTAACGTCCATGCTACTGCTACGTGATGA 518
Db 259 TGGTTGTTGATAATCCGGTGTGGTAATGACGGTGTGGTAATGAGATGTGTA 200

Qy 519 TGGAGTAACTACTGATTATGT 539
Db 199 TGATGATGTAATGATAGTAT 179

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